



## SEQUENCE LISTING

<110> Jalkanen, Markku  
Darwish, Kamel El  
Lindhahl, Ulf  
Li, Jin-Ping

<120> Glucuronyl C5-Epimerase, DNA Encoding the Same and Uses Thereof

<130> 1708.0280002

<140> US 10/005,647

<141> 2001-12-07

<150> US 60/304,180

<151> 2000-12-08

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<160> 11

<170> PatentIn version 3.2

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<211> 1854

<212> DNA

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gat gag cac acc att aaa ggg aga cga gag ggg aat gaa gtt ttc ctt	Asp Glu His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu					115 120					125					384
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aat cta acc gag aaa ccc cct cac ata gaa gta tat gaa aca gca gaa	Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu					225 230					235 240					720
gac agg gac aga aac atc aga cct aat gaa tgg act gtg ccc aag ggg	Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly					245 250					255					768
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cag ttt att gct cca gaa acc agt gaa ggt gtg tct ttg cag ctg gga	Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly					275 280					285					864
aac aca aaa gac ttc att att tca ttt gac ctc aag ctt tta aca aat	Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn					290 295					300					912
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Gln	Asp	Glu	Lys	Gly	Gly	Trp	Pro	Ile	Met	Val	Thr	Arg	Lys	Leu	Gly	
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Glu	Gly	Phe	Lys	Ser	Leu	Glu	Pro	Gly	Trp	Tyr	Ser	Ala	Met	Ala	Gln	
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Ser	Asp	Lys	Ala	Ile	Gln	Phe	Pro	Arg	His	Leu	Ser	Ser	Gly	Phe	Arg	
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Val	Asp	Gly	Leu	Glu	Lys	Arg	Ser	Ala	Ala	Ser	Glu	Ser	Asn	His	Tyr	
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Ala	Asn	His	Ile	Ala	Lys	Gln	Gln	Ser	Glu	Glu	Ala	Phe	Pro	Gln	Glu	
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Ser	Lys	Val	Leu	Gly	Leu	Lys	Tyr	Glu	Glu	Ile	Asp	Cys	Leu	Ile	Asn	
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Asp	Glu	His	Thr	Ile	Lys	Gly	Arg	Arg	Glu	Gly	Asn	Glu	Val	Phe	Leu	
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Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val  
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Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys  
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Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser  
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Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr  
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Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys  
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Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr Ala Glu  
 225 230 235 240

Asp Arg Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly  
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Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys  
 260 265 270

Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly  
 275 280 285

Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Leu Leu Thr Asn  
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Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe  
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Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Arg Asp Arg  
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Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr  
 340 345 350

Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr  
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Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu

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385		390		400
Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn				
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Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys Leu Gly				
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Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala Gln				
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Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys Asp				
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Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys Phe				
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Pro Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys His Asp				
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Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly				
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Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly				
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Glu Thr Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu				
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Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile				
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Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg				
	565	570		575
Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr				
	580	585		590
Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser				
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Tyr Leu Lys Gly Ser Arg Ala Lys His Asn				
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Gln Phe Pro Arg His Leu Ser Ser Gly Phe Arg Val Asp Gly Leu Glu
          35          40          45

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```

Lys Arg Ser Ala Ala Ser Glu Ser Asn His Tyr Ala Asn His Ile Ala
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Lys Gln Gln Ser Glu Glu Ala Phe Pro Gln Glu Gln Gln Lys Ala Pro
65          70          75          80

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Pro Val Val Gly Gly Phe Asn Ser Asn Gly Gly Ser Lys Tyr Glu Glu
          85          90          95

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Ile Asp Cys Leu Ile Asn Asp Glu His Thr Ile Lys Gly Arg Arg Glu
          100          105          110

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Gly Asn Glu Val Phe Leu Pro Phe Thr Trp Val Glu Lys Tyr Phe Asp  
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Val Tyr Gly Lys Val Val Gln Tyr Asp Gly Tyr Asp Arg Phe Glu Phe  
 130 135 140

Ser His Ser Tyr Ser Lys Val Tyr Ala Gln Arg Ser Pro Asp Gly Val  
 145 150 155 160

Phe Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys  
 165 170 175

Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro  
 180 185 190

Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His  
 195 200 205

Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Arg  
 210 215 220

Asp Arg Asn Ile Arg Pro Asn Glu Trp Thr Val Pro Lys Gly Cys Phe  
 225 230 235 240

Met Ala Ser Val Ala Asp Lys Ser Arg Ser Thr Asn Val Lys Gln Phe  
 245 250 255

Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly Asn Thr  
 260 265 270

Lys Asp Phe Ile Ile Ser Phe Asp Asn Gly Ser Val Ser Val Val Leu  
 275 280 285

Glu Thr Thr Glu Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn  
 290 295 300

Thr Gln Leu Ile Ala Phe Arg Asp Arg Asp Ile Tyr Tyr Gly Ile Gly  
 305 310 315 320

Pro Arg Thr Ser Trp Ser Thr Val Thr Asp Leu Arg Lys Gly Val Gly  
 325 330 335

Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Lys Ile Met Pro Lys Lys  
 340 345 350

Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr  
 355 360 365

Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp  
 370 375 380

Leu Val Arg Asn Gln Asp Glu Lys Gly Ile Met Val Thr Arg Lys Leu  
 385 390 395 400

Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala  
 405 410 415

Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys  
 420 425 430

Asp Tyr Val Phe Leu Ser Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys  
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Phe Pro Ser Glu Gln His Gly Val Lys Ala Val His Asp Trp Tyr Glu  
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Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly Phe Met Tyr  
 465 470 475 480

Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly Glu Thr Leu  
 485 490 495

Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu Ser Leu Lys  
 500 505 510

Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr His Phe Met Leu  
 515 520 525

Gly Ile Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile  
 530 535 540

Asn Gln Leu Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys  
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Glu Phe Val Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys  
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His Asn

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Phe Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg Val Lys  
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 35 40 45

Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His  
 50 55 60

Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Arg  
 65 70 75 80

Asp Lys Asn Ser Lys Pro Asn Asp Trp Thr Val Pro Lys Gly Cys Phe  
 85 90 95

Met Ala Ser Val Ala Asp Lys Ser Arg Phe Thr Asn Val Lys Gln Phe  
 100 105 110

Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln Leu Gly Asn Thr  
 115 120 125

Lys Asp Phe Ile Ile Ser Phe Asp Asn Gly Ser Val Ser Val Val Leu  
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Glu Thr Thr Glu Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn  
 145 150 155 160

Thr Gln Leu Ile Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly  
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Pro Arg Thr Ser Trp Ser Thr Val Thr Asp Leu Arg Lys Gly Val Gly  
 180 185 190

Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys Lys  
 195 200 205

Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr  
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Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp  
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Leu Val Arg Asn Gln Asp Glu Lys Gly Ile Met Val Thr Arg Lys Leu  
 245 250 255

Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met Ala  
 260 265 270

Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr Lys  
 275 280 285

Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr Ala Pro Tyr Lys  
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 305 310 315 320

Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu Asn Gly Phe Met Tyr  
 325 330 335

Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr Ala Gly Glu Lys Leu  
 340 345 350

Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly Met Glu Ser Leu Lys  
 355 360 365

Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr His Phe Met Leu  
 370 375 380

Gly Ile Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile  
 385 390 395 400

Asn Gln Leu Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys  
 405 410 415

Glu Phe Val Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys  
 420 425 430

His Asn

<210> 6  
 <211> 569  
 <212> PRT

<213> Homo sapiens

<400> 6

Asn Tyr Lys Thr Leu Ile Ile Ile Cys Ala Leu Phe Thr Leu Val Thr  
1 5 10 15

Val Leu Leu Ser Asp Lys Ala Ile Gln Phe Pro Arg Arg Ser Ser Ser  
20 25 30

Gly Phe Arg Val Asp Gly Phe Glu Lys Arg Ala Ala Ala Ser Glu Ser  
35 40 45

Asn Asn Tyr Met Asn His Val Ala Lys Gln Gln Ser Glu Glu Ala Phe  
50 55 60

Pro Gln Glu Gln Gln Lys Ala Pro Pro Val Val Gly Gly Phe Asn Ser  
65 70 75 80

Asn Val Gly Ser Lys Tyr Glu Glu Ile Asp Cys Leu Ile Asn Asp Glu  
85 90 95

His Thr Ile Lys Gly Arg Arg Glu Gly Asn Glu Val Phe Leu Pro Phe  
100 105 110

Thr Trp Val Glu Lys Tyr Phe Asp Val Tyr Gly Lys Val Val Gln Tyr  
115 120 125

Asp Gly Tyr Asp Arg Phe Glu Phe Ser His Ser Tyr Ser Lys Val Tyr  
130 135 140

Ala Gln Arg Ala Pro Asp Gly Val Phe Met Ser Phe Glu Gly Tyr Asn  
145 150 155 160

Val Glu Val Arg Asp Arg Val Lys Cys Ile Ser Gly Val Glu Gly Val  
165 170 175

Pro Leu Ser Thr Gln Trp Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln  
180 185 190

Ile Ala Gln Tyr Gly Leu Ser His Tyr Ser Lys Asn Leu Thr Glu Lys  
195 200 205

Pro Pro His Ile Glu Val Tyr Arg Asp Lys Asn Lys Pro Asn Asp Trp  
210 215 220

Thr Val Pro Lys Gly Cys Phe Met Ala Asn Val Ala Asp Lys Ser Arg

225		230		235		240
Phe Thr Asn Val	Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val					
	245		250			255
Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Asn						
	260		265			270
Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln Leu Phe						
	275		280			285
Thr Ile His Tyr Val Ser Asn Ala Gln Leu Ile Ala Phe Lys Glu Arg						
	290		295			300
Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr Val Thr						
	305		310			315
Asp Leu Arg Lys Gly Val Gly Leu Ser Asn Thr Lys Ala Val Lys Pro						
	325		330			335
Thr Lys Ile Met Pro Lys Lys Val Val Arg Leu Ile Ala Lys Gly Lys						
	340		345			350
Gly Phe Leu Asp Asn Ile Thr Ile Ser Thr Thr Ala His Met Ala Ala						
	355		360			365
Phe Phe Ala Ala Ser Asp Trp Leu Val Arg Asn Gln Asp Glu Lys Gly						
	370		375			380
Ile Met Val Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro						
	385		390			395
Gly Trp Tyr Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val						
	405		410			415
Arg Ala Tyr Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu						
	420		425			430
Arg Ala Thr Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys						
	435		440			445
Ala Val His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe						
	450		455			460
Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys						
	465		470			475
						480

Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu  
                   485                  490                  495

Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly  
                   500                  505                  510

Ser Gly Thr His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Arg Trp  
                   515                  520                  525

Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu Ser Thr Ile  
                   530                  535                  540

Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp Lys Ser Tyr  
                   545                  550                  555                  560

Leu Lys Gly Ser Arg Ala Lys His Asn  
                   565

<210> 7  
 <211> 576  
 <212> PRT  
 <213> Drosophila sp.

<400> 7

Met Ser Lys Tyr Leu Ser Ser Gln Arg Asp Ala Leu Ser Ala Pro Ala  
   1                  5                  10                  15

Leu Pro Val Ser Arg Glu Asn Arg Glu Pro Pro Lys Phe Gln Gly Val  
                   20                  25                  30

Lys Gln Arg Glu Pro Leu Val Phe Phe Ile Met Arg Leu Asn Leu Lys  
                   35                  40                  45

Ala Val Leu Leu Val Leu Thr Val Ala Val Val Val Ile Thr Leu Gly  
                   50                  55                  60

Val Ala Phe Ser Phe Ser Pro Asp Phe Val Arg Pro Leu Asp Arg Ser  
   65                  70                  75                  80

Ala Arg Gln Ser Ser Ser Gly Gly Glu His Asp Ile Glu Cys Ser Ile  
                   85                  90                  95

Asn Gln Glu Tyr Thr Val His Cys Lys Arg Asp Glu Asn Ala Asn Glu  
                   100                  105                  110

Val Tyr Val Pro Phe Ser Phe Leu Arg Asn Tyr Phe Asp Val Ser Gly  
 115 120 125  
 Ala Val Ser Thr Asn Ser Asn Glu Val Ala Lys Phe Asn Trp Val His  
 130 135 140  
 Ser Thr Ala Lys Val Asn Leu Pro Arg Gly Lys Arg Gly Val Tyr Met  
 145 150 155 160  
 Tyr Phe Glu Asn Tyr Asn Val Glu Val Arg Asp Arg Val Lys Cys Ile  
 165 170 175  
 Ser Ala Ala Glu Gly Val Pro Val Ser Thr Gln Trp Glu Lys Arg Gly  
 180 185 190  
 Tyr Phe Tyr Pro Thr Gln Ile Ala Gln Phe Ala Leu Ser His Tyr Ser  
 195 200 205  
 Lys Asn Leu Thr Glu Pro Ala Pro Arg Val Arg Val Leu Gly Asp Gly  
 210 215 220  
 Asn Gln Met Glu Trp Ser Thr Pro Lys Thr Ser Asn Met Thr Arg Ile  
 225 230 235 240  
 Trp His His Lys Phe Asn Thr Ser Val Val Gln Phe Glu Thr Ala Pro  
 245 250 255  
 Gly Tyr Glu Gly Val Ile Ser Ile Ala Leu Asn Gln Thr Leu Asp Leu  
 260 265 270  
 Leu Leu Ser Val Asp Asn Ser Ser Ser Leu Met Ile Thr Val Gln Asn  
 275 280 285  
 Arg Asp Thr Arg His Asn Tyr Ser Leu His Tyr Ile Pro Ala Asp Leu  
 290 295 300  
 Leu Leu Ser Val Gln Asp Thr Asn Ile Tyr Tyr Gly Leu Gly Gly Ser  
 305 310 315 320  
 Ala Leu Asn Lys Trp Arg His Ile Thr Asp Leu Gln Lys Gly Ile Met  
 325 330 335  
 Gly Asp Lys Arg Ser Pro Leu Lys Ile Arg Arg Ser Asp Leu Glu Val  
 340 345 350  
 Ile Ser Ile Gly Phe Leu Gly Leu Gly Phe Phe Asp Asn Ile Thr Leu



355	360	365
Ser Thr Ser Asp His Leu Ala His Phe Tyr Asp Ala Ala Glu Trp Phe		
370	375	380
Val His Asn Gln Asp Pro Lys Thr Gly Val Arg Arg Ser Leu Asn Gly		
385	390	400
Phe Ala Glu Leu Arg Pro Gly Trp Ile Ser Ala Met Gly Gln Gly His		
	405	410 415
Ala Ile Ser Val Leu Ala Arg Ala Tyr Trp His Ser Gly Gly Asp Glu		
	420	425 430
Arg Tyr Leu Arg Ala Ala Ala Ala Gly Leu Gln Pro Tyr Arg Val Tyr		
	435	440 445
Ser Arg Asp Gly Gly Val Leu Ala Gln Phe Tyr Trp Tyr Glu Glu Tyr		
450	455	460
Pro Thr Thr Pro Pro Ser Tyr Val Leu Asn Gly Phe Ile Tyr Ser Leu		
465	470	475 480
Leu Gly Leu Tyr Asp Leu Asn Ser Thr Ala Pro Gly Lys Ile Ala Arg		
	485	490 495
Glu Ala Gly Lys Leu Phe Ala Gln Gly Met His Ser Leu Lys Lys Met		
	500	505 510
Leu Leu Leu Phe Asp Thr Gly Ser Gly Thr His Leu Ser Leu Gly Val		
	515	520 525
Ala Pro Asn Leu Ala Arg Trp Asp Tyr His Ala Thr His Val Asn Gln		
	530	535 540
Leu Leu Leu Leu Ala Thr Ile Asp Ser Asp Pro Leu Ile Ala Gln Thr		
545	550	555 560
Ala Glu Arg Trp Lys Gly Tyr Met Phe Gly Arg Arg Ala Lys His Asn		
	565	570 575

<210> 8  
 <211> 599  
 <212> PRT  
 <213> C. elegans  
 <400> 8

Met	Val	Leu	Val	Ser	Leu	Lys	Pro	Phe	Asn	Ile	Phe	Ser	Leu	Lys	Pro	1	5	10	15
Met	Lys	Cys	Leu	Arg	Trp	Arg	Ser	Asn	Arg	His	Arg	Ile	Tyr	Leu	Leu	20	25	30	
Val	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Leu	Arg	His	Leu	Thr	Gln	Glu	Glu	35	40	45	
Ser	Arg	Ile	Asp	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Gln	Val	Asp	Val	Asn	50	55	60	
Glu	Asp	Asp	Lys	Lys	Ile	Glu	Cys	Glu	Pro	Pro	Gly	Ser	Ile	Glu	Ser	65	70	75	80
Lys	Cys	Ile	Ala	Asp	Asn	Gly	Lys	Ser	Met	Lys	Cys	Trp	Lys	Asp	Glu	85	90	95	
Glu	Asp	Val	Tyr	Phe	Pro	Val	Ser	Tyr	Leu	Lys	Lys	Arg	Phe	Asp	Met	100	105	110	
Thr	Gly	Lys	Leu	Gly	Lys	Asp	Gly	Ser	Thr	Phe	Glu	Leu	Tyr	Thr	Ser	115	120	125	
Tyr	Ala	Lys	Met	Arg	Ser	Pro	Asp	Leu	Gly	Pro	Phe	Gly	His	Phe	Ser	130	135	140	
Thr	Tyr	Ser	Val	Glu	Thr	Arg	Asp	Arg	Val	Arg	Cys	Val	Ser	Ala	Lys	145	150	155	160
Thr	Asp	Val	Pro	Met	Ser	Thr	Gln	Trp	Asp	Pro	Ile	Pro	Tyr	Tyr	Tyr	165	170	175	
Pro	Ile	Gln	Ile	Ser	Gln	Tyr	Gly	Leu	Gln	His	Tyr	Ser	Arg	Met	Lys	180	185	190	
Leu	Asp	Ser	Ile	Ser	Asn	Lys	Ser	Glu	Ala	Ser	Pro	Lys	Asp	Asp	Val	195	200	205	
Ile	Asn	Ser	Lys	Glu	Trp	Lys	Gly	Ala	Ala	Gly	Met	His	Glu	Thr	Thr	210	215	220	
Glu	Arg	Leu	Phe	Phe	Asn	Asp	Glu	Gln	Met	Gly	Lys	Val	Val	Asn	Ile	225	230	235	240

Ser Ala Gly Ala Ala Leu Ala Asn Ala Gly Ala Tyr Val Tyr Leu Asp  
 245 250 255

Lys Ser Pro Asp Leu His Val Ile Ser Phe Asp Ala Asn Ser Ser Phe  
 260 265 270

Thr Val Leu Ala Lys Met Lys Gln Asp Asp Leu Leu Val Leu Ile Asn  
 275 280 285

Tyr Val Tyr Ser Glu Gly Asn Gly Lys Cys Val Trp Gln Glu Glu Glu  
 290 295 300

Arg Ile Ser Asp Asp Tyr Ile Val Gln Lys Pro Lys Lys Asp Gly Gln  
 305 310 315 320

Val Ser Tyr Ser Tyr Ser Tyr Ile Gly Asn Ser Pro Ile Gly Glu Trp  
 325 330 335

Ser Thr Val Thr Asp Val Ala Arg Ala Leu Ser Ser Gly Asp Asn Arg  
 340 345 350

Lys Lys Asp Asp Asn Val Val Leu His Ala Gly Asp Leu Arg Leu Val  
 355 360 365

Ser Leu Gly Phe Arg Gly Glu Leu Thr Val Lys Gln Lys Ile Thr Gln  
 370 375 380

Arg Arg Glu Gln His Ser His Ala Phe Tyr Ala Ala Ala Asp Trp Leu  
 385 390 395 400

Val Lys Asn Gln Asn Asp Arg Gly Val Glu Arg Ser Ile Ala Glu Arg  
 405 410 415

Lys Leu Val Leu Pro Pro Gly Trp His Ser Ala Met Ala Gln Gly His  
 420 425 430

Gly Ile Ser Val Leu Thr Arg Ala Phe Lys His Phe Asn Asp Glu Lys  
 435 440 445

Tyr Leu Lys Ser Ala Ala Lys Ala Leu Lys Leu Phe Lys Ile Asn Ser  
 450 455 460

Ser Asp Gly Gly Val Arg Gly Glu Ile Trp Tyr Glu Glu Tyr Pro Thr  
 465 470 475 480

Thr Pro Gly Ser Phe Val Leu Asn Gly Phe Leu Tyr Ser Leu Ile Gly

Arg Lys Cys Phe Tyr Lys Tyr Phe Lys Leu Lys Asp Lys Asn Pro Lys  
85 90 95

Glu Ala Glu Arg Tyr Leu Lys Arg Gly Leu Phe Leu Thr Glu Tyr Leu  
                   100                  105                  110

Ile Ser Gln Ala Asp Lys Glu Thr Ala Glu Val Asp Glu Lys Asn Ile  
           115                  120                  125

Thr Phe Ile Val Trp Arg Tyr Asn Phe Glu Phe Pro Asn Leu Ser Lys  
       130                  135                  140

Gly Trp Arg Gly Ala Leu Cys Gln Ala Gly Cys Leu Lys Thr Leu Tyr  
   145                  150                  155                  160

Leu Ala Tyr Glu Ala Thr Gly Asp Glu Arg Tyr Leu Asn Tyr Ala Asn  
                   165                  170                  175

Leu Ala Ile Asn Ala Phe Lys Val Pro Val Glu Lys Gly Gly Leu Leu  
           180                  185                  190

Lys Ile Arg Ile Tyr Tyr Trp Phe Pro Glu Tyr Ala Ser Glu Asn Pro  
           195                  200                  205

Pro Tyr Val Leu Asn Gly Phe Ile  
       210                  215

<210> 10  
 <211> 174  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Tag that preceded each recombinant construct

<220>  
 <221> CDS  
 <222> (1)..(174)

<400> 10  
 atg act att ctc tgc tgg ctt gcg ctg ttg tca aca ctt acc gcc gtg 48  
 Met Thr Ile Leu Cys Trp Leu Ala Leu Leu Ser Thr Leu Thr Ala Val  
 1                  5                  10                  15  
  
 aac gca gac tac aag gac gac gat gac aag cgg ccg cat gcg gaa ttc 96  
 Asn Ala Asp Tyr Lys Asp Asp Asp Lys Arg Pro His Ala Glu Phe  
           20                  25                  30  
  
 atg cgg ggt tct cat cac cat cac cat cac gat tac gat atc cca acg 144  
 Met Arg Gly Ser His His His His His His Asp Tyr Asp Ile Pro Thr  
           35                  40                  45  
  
 acc gaa aac ctg tat ttt cag ggc gcc atg 174  
 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met

50

55

&lt;210&gt; 11

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Tag that preceded each recombinant construct

&lt;400&gt; 11

Met	Thr	Ile	Leu	Cys	Trp	Leu	Ala	Leu	Leu	Ser	Thr	Leu	Thr	Ala	Val
1				5					10					15	

Asn	Ala	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Arg	Pro	His	Ala	Glu	Phe
			20					25					30		

Met	Arg	Gly	Ser	His	His	His	His	His	His	Asp	Tyr	Asp	Ile	Pro	Thr
			35					40				45			

Thr	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ala	Met
50						55			